Group D: claim 28, drawn to a method of identifying a compound or agent that binds a CLASP-2 polypeptide comprising contacting a CLASP-2 polypeptide with the compounds and detecting the presence of a complex, classified in class 435, subclass 4, for example.

Group E: claim 29, drawn to a method of detecting a CLASP-2 polypeptide comprising contacting the sample with an antibody and determining whether a complex has been formed, classified in class 435, subclass 7.1.

Group F: claim 30, drawn to a method of detecting a CLASP-2 polypeptide [*sic*, polynucleotide] in a sample comprising contacting the sample with a polynucleotide and determining whether a hybridization complex has been formed, classified in class 435, subclass 6.

Group G: claim 31, drawn to a method of detecting a CLASP-2 nucleotide [*sic*, polynucleotide] in a sample comprising using a polynucleotide in an amplification process and determining whether a specific amplification product has been formed, classified in class 435, subclass 6.

Group H: claims 33-35, drawn to a method of inhibiting an immune response in a subject comprising interfering with the expression of a CLASP-2 gene, interfering with the ability of a CLASP-2 protein to bind another cell, and interfering with the ability of a CLASP-2 protein to bind another protein, classified in class 435, subclass 4.

Group I: claim 36, drawn to a method of inhibiting an immune response in a subject comprising administering to the subject a therapeutically effective amount of an antibody which specifically binds a polypeptide, classified in class 424, subclass 139.1.

Group J: claims 37-39, drawn to a method of preventing or treating a CLASP-2-mediated autoimmune disease comprising administering to a subject in need thereof a therapeutically effective amount of a polynucleotide, classified in class 514, subclass 44.

Group K: claims 37-39, drawn to a method of preventing or treating a CLASP-2-mediated autoimmune disease comprising administering to a subject in need thereof a therapeutically effective amount of a polypeptide, classified in class 512, subclass 2.

Group L: claims 37-39, drawn to a method of preventing or treating a CLASP-2-mediated autoimmune disease comprising administering to a subject in need thereof a therapeutically effective amount of an antibody, classified in class 424, subclass 130.1.

In compliance with the requirement, Applicants elect to prosecute the invention of Group A, claims 1-6, 8-17 and 32. This election is made with traverse.

Applicants respectfully request redefinition of the groups in the interest of administrative efficiency and consistent with art recognized classifications. In particular, Applicants request the following: Combination of Groups A, F and G, drawn to polynucleotides (including a vector, a host cell system, a method of producing a polypeptide, and a pharmaceutical composition); a method of detecting a polynucleotide in a sample by contacting the sample with a polynucleotide to determine whether a hybridization complex has been formed; and a method of detecting a polynucleotide by using a polynucleotide in an amplification process; respectively, into one group. Applicants respectfully assert that closely related isoforms of polynucleotides can be searched together, irrespective of their method of use. The suggested combination is believed to be more consistent with accepted use and Applicants respectfully request adaptation. Applicants also point out that claim 30 erroneously recites "a method of detecting a CLASP-2 *polypeptide* in a sample" which reflects an unintentional error. Instead, the claim should read "a method of detecting a CLASP-2 *polynucleotide* in a sample". No new matter is introduced by this correction. Further, Applicants point out that claim 31 erroneously recites "detecting a CLASP-2 *nucleotide*" which also reflects an unintentional error. Instead, the claim should refer to "detecting a CLASP-2 *polynucleotide*". No new matter is introduced by this correction.

Further, the Examiner required restriction of groups 1-4 as they pertain to each of the nucleotide sequences of SEQ ID NOS: 1, 3, 5, or 9. The Examiner states that restriction is deemed proper because each of SEQ ID NOS: 1, 3, 5, or 9 is a unique nucleotide sequence, requiring a unique search of the prior art. The Examiner also states that the searching of all of the sequences in a single patent application would provide an

undue search burden on the Examiner and the USPTO's resources because of the non-coextensive nature of these searches. Applicants respectfully suggest that an election would be more appropriate with respect to accepted procedure.

In compliance with the requirement, Applicants elect to prosecute SEQ ID NO: 1. This election is made with traverse. Applicants respectfully clarify that SEQ ID NOS: 1, 3, 5 and 9 cover isoforms of human CLASP-2 (hCLASP-2) cDNA. Specifically, SEQ ID NOS: 1, 3, 5 and 9 cover hCLASP-2A, hCLASP-2B, hCLASP-2C, and hCLASP-2E, respectively. Such closely related nucleotide sequences can be searched together without placing an undue search burden on the Examiner or the USPTO's resources. Applicants refer the Examiner to Figures 11A, 11B and 11C of the specification, showing drawings related to the sequences and their similarity. In fact, MPEP 808.02 states the following: "Where, however, the classification is the same and the field of search is the same and there is no clear indication of separate future classification and field of search, no reasons exist for dividing among related inventions."[1] Thus, Applicants would greatly appreciate if the Examiner would reconsider the restriction requirement and upon reconsideration decide to examine SEQ ID NOS: 1, 3, 5 and 9 together in light of their closely related nature.

In support of their argument, Applicants further cite *In re Kuehl*:

> The constitutional purpose of the patent system is promoted by encouraging applicants to claim, and therefore to describe in the manner required by 35 U.S.C. §112, all aspects of what they regard as their inventions, regardless of the number of statutory classes involved. Dependent claims to the use of a new composition in the same application with claims to the composition do not materially increase the scope of protection of an applicant's inchoate patent property under 35 U.S.C. §154, which already includes the right to exclude others from making, using, or selling the composition by allowance of claims thereon, but they do tend to increase the wealth of technical knowledge disclosed in the patent by encouraging description of the use aspect of the applicant's invention in the manner required by 35 U.S.C. §112, paragraph one.[2]

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[1] MPEP 808.02 Related Inventions; (C) A different Field of search
[2] *In re Kuehl*, 475 F.2d 658, 177 USPQ 250, 256 (CCPA 1973)

Further, the Examiner required restriction of a PDZ domain species such as PSD95, DLG1 or neDLG. As discussed *supra*, an election would be more appropriate with respect to accepted procedure. In compliance with the requirement, Applicants elect to prosecute DLG1. This election is made with traverse. Applicants respectfully clarify that PSD95, DLG1 and neDLG are closely related PDZ domains. The specification states the following on page 28: "Biochemical evidence that CLASP-2 interacts with the PDZ domains of three closely related proteins is shown in FIG 9A-D. FIG. 9A demonstrates the specificity of the interaction, as the C-terminal 20 amino acids of CLASP-2 bind to PSD-95, NeDLG, and DLG1, but not to the PDZ domains of the TIAM-1 protein. FIG. 9B demonstrates the affinity of the interaction." Applicants refer the Examiner to Figures 9A and 9B. In light of the domain similarity, it would not place an undue search burden on the Examiner to examine the PDZ domains together. Applicants would, thus, greatly appreciate if the Examiner would reconsider this restriction requirement.

In summary, Applicants elect Group A, SEQ ID NO: 1, and DLG1 in compliance with the requirement. These elections are made with traverse. Applicants request redefinition of the groups such as the combination of Groups A, F and G into one group; the combination of SEQ ID NOS: 1, 3, 5 and 9 into one group; and the combination of PSD95, DLG1 and neDLG into one group.

Respectfully submitted,

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